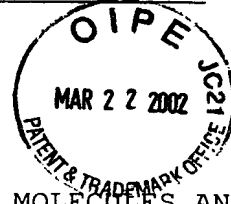


IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Mary Cismowski et al.  
Serial No.: 09/709,103  
Filed : November 8, 2000  
For : AGS PROTEINS AND NUCLEIC ACID MOLECULES AND USES  
THEREFOR



1185 Avenue of the Americas  
New York, New York 10036  
March 18, 2002

U.S. Patent and Trademark Office  
Box Sequence, P.O. Box 2327  
Arlington, VA 22202

Sir:

STATEMENT IN ACCORDANCE WITH 37 C.F.R. §1.821(f)

In accordance with 37 C.F.R. §1.821(f), I hereby certify that the computer readable form containing the nucleic acid and/or amino acid sequences required by 37 C.F.R. §1.821(e) attached hereto has the same information as the paper copy of the "Sequence Listing" submitted herewith as **Exhibit D** in connection with the above-identified application.

I hereby declare that all statements made herein are of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code and that such wilful false statements may jeopardize the validity of the application or any patent issued thereon.

Respectfully submitted,

Joseph B. Crystal  
Joseph B. Crystal  
Cooper & Dunham LLP  
1185 Avenue of the Americas  
New York, New York 10036  
(212) 278-0400

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☒ 7. Other: The statement in accordance with 37 C.F.R. 1.821 (f) filed 3/22/02 does not include a statement of "no new matter". (see 37 CFR 1.821 (g)).

**Applicant Must Provide:**

- ☐ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

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<110> Cismowski, Mary  
Duzic, Emir

<130> 60388-A-PCT-US

<141> 2000-11-08

<170> PatentIn version 3.1

<213> Homo Sapien

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Phe Glu Asp Ala Tyr Thr Pro Thr Ile Glu Asp Phe His Arg Lys Phe	
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Tyr Ser Ile Arg Gly Glu Val Tyr Gln Leu Asp Ile Leu Asp Thr Ser	
65 70 75 80	
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Asp Val Phe Ile Leu Val Phe Ser Leu Asp Asn Arg Asp Ser Phe Glu	
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Glu Val Gln Arg Leu Arg Gln Gln Ile Leu Asp Thr Lys Ser Cys Leu	
115 120 125	
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Lys Asn Lys Thr Lys Glu Asn Val Asp Val Pro Leu Val Ile Cys Gly	
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Asn Lys Gly Asp Arg Asp Phe Tyr Arg Glu Val Asp Gln Arg Glu Ile	
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gcc atg gcc aag ctg ccc agc gag atg agc cca gac ctg cac cgc aag	624
Ala Met Ala Lys Leu Pro Ser Glu Met Ser Pro Asp Leu His Arg Lys	
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Val Ser Val Gln Tyr Cys Asp Val Leu His Lys Lys Ala Leu Arg Asn	
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225 230 235 240	
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Asp Ala Phe Gly Ile Val Ala Pro Phe Ala Arg Arg Pro Ser Val His	
245 250 255	
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Ser Asp Leu Met Tyr Ile Arg Glu Lys Ala Ser Ala Gly Ser Gln Ala	
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<212> PRT

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Lys Asn Lys Thr Lys Glu Asn Val Asp Val Pro Leu Val Ile Cys Gly  
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Glu Gln Leu Val Gly Asp Asp Pro Gln Arg Cys Ala Tyr Phe Glu Ile  
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 210 215 220

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 225 230 235 240

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 Met Lys Leu Ala Ala Met Ile  
 1 5  
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 Lys Lys Met Cys Pro Ser Asp Ser Glu Leu Ser Ile Pro Ala Lys Asn  
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Cys Tyr Arg Met Val Ile Leu Gly Ser Ser Lys Val Gly Lys Thr Ala	
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Ile Val Ser Arg Phe Leu Thr Gly Arg Phe Glu Asp Ala Tyr Thr Pro	
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Thr Ile Glu Asp Phe His Arg Lys Phe Tyr Ser Ile Arg Gly Glu Val	
60 65 70	
tac cag ctc gac atc ctc gac acg tcc ggc aac cac ccg ttc ccc gcc	414
Tyr Gln Leu Asp Ile Leu Asp Thr Ser Gly Asn His Pro Phe Pro Ala	
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Met Arg Arg Leu Ser Ile Leu Thr Gly Asp Val Phe Ile Leu Val Phe	
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Gln Ile Leu Asp Thr Lys Ser Cys Leu Lys Asn Lys Thr Lys Glu Asn	
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155 160 165	
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Glu Met Ser Pro Asp Leu His Arg Lys Val Ser Val Gln Tyr Cys Asp	
200 205 210 215	
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Pro Phe Ala Arg Arg Pro Ser Val His Ser Asp Leu Met Tyr Ile Arg	
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 Ile Ser  
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ctccccggcga tccgccccca gcaactgggga ggcgccactg aaccgagaag ggacgggtcat 1166

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Phe Glu Asp Ala Tyr Thr Pro Thr Ile Glu Asp Phe His Arg Lys Phe  
 50 55 60



Tyr Ser Ile Arg Gly Glu Val Tyr Gln Leu Asp Ile Leu Asp Thr Ser  
65 70 75 80

Gly Asn His Pro Phe Pro Ala Met Arg Arg Leu Ser Ile Leu Thr Gly  
85 90 95

Asp Val Phe Ile Leu Val Phe Ser Leu Asp Asn Arg Asp Ser Phe Glu  
100 105 110

Glu Val Gln Arg Leu Arg Gln Gln Ile Leu Asp Thr Lys Ser Cys Leu  
115 120 125

Lys Asn Lys Thr Lys Glu Asn Val Asp Val Pro Leu Val Ile Cys Gly  
130 135 140

Asn Lys Gly Asp Arg Asp Phe Tyr Arg Glu Val Asp Gln Arg Glu Ile  
145 150 155 160

Glu Gln Leu Val Gly Asp Asp Pro Gln Arg Cys Ala Tyr Phe Glu Ile  
165 170 175

Ser Ala Lys Lys Asn Ser Ser Leu Asp Gln Met Phe Arg Ala Leu Phe  
180 185 190

Ala Met Ala Lys Leu Pro Ser Glu Met Ser Pro Asp Leu His Arg Lys  
195 200 205

Val Ser Val Gln Tyr Cys Asp Val Leu His Lys Lys Ala Leu Arg Asn  
210 215 220

Lys Lys Leu Leu Arg Ala Gly Ser Gly Gly Gly Gly Gly Asp Pro Gly  
225 230 235 240

Asp Ala Phe Gly Ile Val Ala Pro Phe Ala Arg Arg Pro Ser Val His  
245 250 255

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<223> Xaa at position 8 may be Serine or Threonine acid.

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<223> Xaa at position 3 may be any amino acid.

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<223> The C-terminal CAAX.

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<221> MISC\_FEATURE

<222> (4)..(4)

<223> Xaa at position 4 may be any amino acid

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<211> 7

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<213> Homo Sapiens

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Leu Ala Ala Leu Pro His Ser Cys Leu Glu Arg Ala Lys Glu Ile Lys  
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Ile Lys Leu Gly Ile Leu Leu Gln Lys Pro Asp Ser Val Gly Asp Leu  
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Val Ile Pro Tyr Asn Glu Lys Pro Glu Lys Pro Ala Lys Thr Gln Lys  
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Thr Ser Leu Asp Glu Ala Leu Gln Trp Arg Asp Ser Leu Asp Lys Leu  
55 60 65

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Leu Gln Asn Asn Tyr Gly Leu Ala Ser Phe Lys Ser Phe Leu Lys Ser  
70 75 80

gaa ttc agt gag gaa aac ctt gag ttc tgg att gcc tgt gag gat tac 344  
Glu Phe Ser Glu Glu Asn Leu Glu Phe Trp Ile Ala Cys Glu Asp Tyr  
85 90 95 100

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Lys Lys Ile Lys Ser Pro Ala Lys Met Ala Glu Lys Ala Lys Gln Ile  
105 110 115

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Tyr Glu Glu Phe Ile Gln Thr Glu Ala Pro Lys Glu Val Asn Ile Asp  
120 125 130

cac ttc act aag gac atc aca atg aag aac ctg gtg gaa cct tcc ctg 488  
His Phe Thr Lys Asp Ile Thr Met Lys Asn Leu Val Glu Pro Ser Leu  
135 140 145

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Ser Ser Phe Asp Met Ala Gln Lys Arg Ile His Ala Leu Met Glu Lys  
150 155 160

gat tct ctg cct cgc ttt gtg cgc tct gag ttt tat cag gag tta atc 584  
Asp Ser Leu Pro Arg Phe Val Arg Ser Glu Phe Tyr Gln Glu Leu Ile  
165 170 175 180

aag tagtaattta gccaggctat gaaatcatcc tgtgagttat ttctccata 637  
Lys

ataaccctgc atttcccatt aatctacata tcttcccaca gcagctttgc tcagtgtac 697

ccacatggga aaaatcccag gggatgttgc ttactttttt tgcccacact gctttggata 757

cttatctact gtccgaaggc cttctttccc cactcaattc ttctgcct gttattaatt 817

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ctaaattggt ctaaaaaaga atattaagtg tggacagacc tatttcaaag gagcttaatt 997  
 gatctcactt gttttagttc tgatccaggg agatcacccc tctaattatt tctgaacttg 1057  
 gttaataaaa gtttataaga tttttatgaa gcagccactg tatgatattt taagcaaata 1117  
 tgttatttaa aatattgatc cttcccttgg accacettca tgttagttgg gtattataaa 1177  
 taagagatac aaccatgaat atattatggt tatacaaaat caatctgaac acaattcata 1237  
 aagatttctc ttttatacct tcctcactgg cccctccac ctgccatag tcaccaaatt 1297  
 ctgttttaaa tcaatgacct aagatcaaca atgaagtatt ttataaatgt atttatgctg 1357  
 ctgactgtg ggtcaaagt ttccattttc aaattattta gaattcttat gagtttaaaa 1417  
 tttgtaaatt tctaaatcca atcatgtaa atgaaactgt tgctccattg gagtagtctc 1477  
 ccacctaaat atcaagatgg ctatatgcta aaaagagaaa atatggtcaa gtctaaaatg 1537  
 gctaattgtc ctatgatgct attatcatag actaatgaca tttatcttca aaacacccaa 1597  
 ttgtctttag aaaaattaat gtgattacag gtagaggcct tctaggtgag acacttttaa 1657  
 ggtacactgc attttgcaaa aaaaaaaaaa aaaa 1691

<210> 25

<211> 181

<212> PRT

<213> Homo Sapiens

<400> 25

Met Cys Lys Gly Leu Ala Ala Leu Pro His Ser Cys Leu Glu Arg Ala  
 1 5 10 15

Lys Glu Ile Lys Ile Lys Leu Gly Ile Leu Leu Gln Lys Pro Asp Ser  
 20 25 30

Val Gly Asp Leu Val Ile Pro Tyr Asn Glu Lys Pro Glu Lys Pro Ala  
 35 40 45

Lys Thr Gln Lys Thr Ser Leu Asp Glu Ala Leu Gln Trp Arg Asp Ser  
 50 55 60

Leu Asp Lys Leu Leu Gln Asn Asn Tyr Gly Leu Ala Ser Phe Lys Ser  
 65 70 75 80

Phe Leu Lys Ser Glu Phe Ser Glu Glu Asn Leu Glu Phe Trp Ile Ala  
 85 90 95

Cys Glu Asp Tyr Lys Lys Ile Lys Ser Pro Ala Lys Met Ala Glu Lys  
100 105 110

Ala Lys Gln Ile Tyr Glu Glu Phe Ile Gln Thr Glu Ala Pro Lys Glu  
115 120 125

Val Asn Ile Asp His Phe Thr Lys Asp Ile Thr Met Lys Asn Leu Val  
130 135 140

Glu Pro Ser Leu Ser Ser Phe Asp Met Ala Gln Lys Arg Ile His Ala  
145 150 155 160

Leu Met Glu Lys Asp Ser Leu Pro Arg Phe Val Arg Ser Glu Phe Tyr  
165 170 175

Gln Glu Leu Ile Lys  
180

<210> 26

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 26

ccagatctaa agatgccgat ttgggcg

27

<210> 27

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 27

ccccatggtt ttatatattgt tgtaaaaagt ag

32

<210> 28

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 28

cgggatccat gtgcaaaggg cttgcaggtc

30

<210> 29

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 29

ccgctcgagt taggcacact gagggacc

28

<210> 30

<211> 41

<212> DNA

<213> Homo Sapiens

<400> 30

agtcggtacc cgcataagatc tgcaggatgc cctttttgac g

41

<210> 31

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 31  
gtacgtcgac ttgattttc agaaacttga tggc

34

<210> 32

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 32  
tggcctcgag atgacaaatt caaaagaaga cg

32

<210> 33

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 33  
atcactgcag ctatgctaca acattccaaa at

32

<210> 34

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 34  
gggtcatgaa actggccgcg atgatcaaga ag

32

<210> 35

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 35

gatagtcgac ctagctgatg acgcagcgct c

31

<210> 36

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 36

cgcattgtca tcctcgtttc gtccaagggt g

31

<210> 37

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 37

ccaccttgga cgaaacgagg atgaccatgc g

31

<210> 38

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 38

ccaaggacaa ggagcgcagc gtcacacagct ag

32

<210> 39

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 39

ctagctgatg acgctgcgct ccttgctcctt gg

32

<210> 40

<211> 837

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

<222> (1) .. (834)

<223>

<400> 40

atg cct gct tct ctc gct ttg ttg cag ccc cga gcc atg atg aag act  
Met Pro Ala Ser Leu Ala Leu Leu Gln Pro Arg Ala Met Met Lys Thr  
1 5 10 15

48

ttg tcc agc ggg aac tgc acg ctc agt gtg ccc gcc aaa aac tca tac  
Leu Ser Ser Gly Asn Cys Thr Leu Ser Val Pro Ala Lys Asn Ser Tyr  
20 25 30

96

cgc atg gtg gtg ctg ggt gcc tct cgg gtg ggc aag agc tcc atc gtg  
Arg Met Val Val Leu Gly Ala Ser Arg Val Gly Lys Ser Ser Ile Val  
35 40 45

144

tct cgc ttc ctc aat ggc cgc ttt gag gac cag tac aca ccc acc atc  
Ser Arg Phe Leu Asn Gly Arg Phe Glu Asp Gln Tyr Thr Pro Thr Ile  
50 55 60

192

gag gac ttc cac cgt aag gta tac aac atc cgc ggc gac atg tac cag Glu Asp Phe His Arg Lys Val Tyr Asn Ile Arg Gly Asp Met Tyr Gln 65 70 75 80	240
ctc gac atc ctg gat acc tct ggc aac cac ccc ttc ccc gcc atg cgc Leu Asp Ile Leu Asp Thr Ser Gly Asn His Pro Phe Pro Ala Met Arg 85 90 95	288
agg ctg tcc atc ctc aca ggg gat gtc ttc atc ctg gtg ttc agc ctg Arg Leu Ser Ile Leu Thr Gly Asp Val Phe Ile Leu Val Phe Ser Leu 100 105 110	336
gat aac cgg gag tcc ttc gat gag gtc aag cgc ctt cag aag cag atc Asp Asn Arg Glu Ser Phe Asp Glu Val Lys Arg Leu Gln Lys Gln Ile 115 120 125	384
ctg gag gtc aag tcc tgc ctg aag aac aag acc aag gag gcg gcg gag Leu Glu Val Lys Ser Cys Leu Lys Asn Lys Thr Lys Glu Ala Ala Glu 130 135 140	432
ctg ccc atg gtc atc tgt ggc aac aag aac gac cac ggc gag ctg tgc Leu Pro Met Val Ile Cys Gly Asn Lys Asn Asp His Gly Glu Leu Cys 145 150 155 160	480
cgc cag gtg ccc acc acc gag gcc gag ctg ctg gtg tcg ggc gac gag Arg Gln Val Pro Thr Glu Ala Glu Leu Leu Val Ser Gly Asp Glu 165 170 175	528
aac tgc gcc tac ttc gag gtg tcg gcc aag aag aac acc aac gtg gac Asn Cys Ala Tyr Phe Glu Val Ser Ala Lys Lys Asn Thr Asn Val Asp 180 185 190	576
gag atg ttc tac gtg ctc ttc agc atg gcc aag ctg cca cac gag atg Glu Met Phe Tyr Val Leu Phe Ser Met Ala Lys Leu Pro His Glu Met 195 200 205	624
agc ccc gcc ctg cat cgc aag atc tcc gtg cag tac ggt gac gcc ttc Ser Pro Ala Leu His Arg Lys Ile Ser Val Gln Tyr Gly Asp Ala Phe 210 215 220	672
cac ccc agg ccc ttc tgc atg cgc cgc gtc aag gag atg gac gcc tat His Pro Arg Pro Phe Cys Met Arg Arg Val Lys Glu Met Asp Ala Tyr 225 230 235 240	720
ggc atg gtc tcg ccc ttc gcc cgc cgc ccc agc gtc aac agt gac ctc Gly Met Val Ser Pro Phe Ala Arg Arg Pro Ser Val Asn Ser Asp Leu 245 250 255	768
aag tac atc aag gcc aag gtc ctt cgg gaa ggc cag gcc cgt gag agg Lys Tyr Ile Lys Ala Lys Val Leu Arg Glu Gly Gln Ala Arg Glu Arg 260 265 270	816
gac aag tgc acc atc cag tga Asp Lys Cys Thr Ile Gln 275	837

<210> 41

<211> 278



<212> PRT

<213> Homo Sapiens

<400> 41

Met Pro Ala Ser Leu Ala Leu Leu Gln Pro Arg Ala Met Met Lys Thr  
1 5 10 15

Leu Ser Ser Gly Asn Cys Thr Leu Ser Val Pro Ala Lys Asn Ser Tyr  
20 25 30

Arg Met Val Val Leu Gly Ala Ser Arg Val Gly Lys Ser Ser Ile Val  
35 40 45

Ser Arg Phe Leu Asn Gly Arg Phe Glu Asp Gln Tyr Thr Pro Thr Ile  
50 55 60

Glu Asp Phe His Arg Lys Val Tyr Asn Ile Arg Gly Asp Met Tyr Gln  
65 70 75 80

Leu Asp Ile Leu Asp Thr Ser Gly Asn His Pro Phe Pro Ala Met Arg  
85 90 95

Arg Leu Ser Ile Leu Thr Gly Asp Val Phe Ile Leu Val Phe Ser Leu  
100 105 110

Asp Asn Arg Glu Ser Phe Asp Glu Val Lys Arg Leu Gln Lys Gln Ile  
115 120 125

Leu Glu Val Lys Ser Cys Leu Lys Asn Lys Thr Lys Glu Ala Ala Glu  
130 135 140

Leu Pro Met Val Ile Cys Gly Asn Lys Asn Asp His Gly Glu Leu Cys  
145 150 155 160

Arg Gln Val Pro Thr Thr Glu Ala Glu Leu Leu Val Ser Gly Asp Glu  
165 170 175

Asn Cys Ala Tyr Phe Glu Val Ser Ala Lys Lys Asn Thr Asn Val Asp  
180 185 190

Glu Met Phe Tyr Val Leu Phe Ser Met Ala Lys Leu Pro His Glu Met  
195 200 205

Ser Pro Ala Leu His Arg Lys Ile Ser Val Gln Tyr Gly Asp Ala Phe  
210 215 220

His Pro Arg Pro Phe Cys Met Arg Arg Val Lys Glu Met Asp Ala Tyr  
225 230 235 240

Gly Met Val Ser Pro Phe Ala Arg Arg Pro Ser Val Asn Ser Asp Leu  
245 250 255

Lys Tyr Ile Lys Ala Lys Val Leu Arg Glu Gly Gln Ala Arg Glu Arg  
260 265 270

Asp Lys Cys Thr Ile Gln  
275

<210> 42

<211> 15

<212> PRT

<213> Homo Sapiens

<400> 42

Asp Thr Lys Ser Cys Leu Lys Asn Lys Thr Lys Glu Asn Val Asp  
1 5 10 15

<210> 43

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 43  
ttctcgcgga tgtacatga

19

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 44

tccaccgcaa gttctactcc

20

<210> 45

<211> 1740

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

<222> (146) .. (988)

<223>

<400> 45

gagcggagcc ggagcccca gcccagaccg cgcccagccc gagcagagcc ctccagccgc 60

tcaccccgcg tgccaccca ggcacctca gccgctctct gcccttctct cggcccgcg 120

cccgccctcg cggccctct gccc atg aaa ctg gcc gcg atg atc aag aag 172  
Met Lys Leu Ala Ala Met Ile Lys Lys  
1 5

atg tgc ccg agc gac tcg gag ctg agt atc ccg gcc aag aac tgc tat 220  
Met Cys Pro Ser Asp Ser Glu Leu Ser Ile Pro Ala Lys Asn Cys Tyr  
10 15 20 25

cgc atg gtc atc ctc ggc tcg tcc aag gtg ggc aag acg gcc atc gtg 268  
Arg Met Val Ile Leu Gly Ser Ser Lys Val Gly Lys Thr Ala Ile Val  
30 35 40

tcg cgc ttc ctc acc ggc cgc ttc gag gac gcc tac acg cct acc atc 316  
Ser Arg Phe Leu Thr Gly Arg Phe Glu Asp Ala Tyr Thr Pro Thr Ile  
45 50 55

gag gac ttc cac cgc aag ttc tac tcc atc cgc ggc gag gtc tac cag 364  
Glu Asp Phe His Arg Lys Phe Tyr Ser Ile Arg Gly Glu Val Tyr Gln  
60 65 70

ctc gac atc ctc gac acg tcc ggc aac cac ccg ttc ccc gcc atg cgg 412  
Leu Asp Ile Leu Asp Thr Ser Gly Asn His Pro Phe Pro Ala Met Arg  
75 80 85

cgc ctc tcc atc ctc aca gga gac gtt ttc atc ctg gtg ttc agt ctg	460
Arg Leu Ser Ile Leu Thr Gly Asp Val Phe Ile Leu Val Phe Ser Leu	
90 95 100 105	
gac aac cgc gac tcc ttc gag gag gtg cag cgg ctc agg cag cag atc	508
Asp Asn Arg Asp Ser Phe Glu Glu Val Gln Arg Leu Arg Gln Gln Ile	
110 115 120	
ctc gac acc aag tct tgc ctc aag aac aaa acc aag gag aac gtg gac	556
Leu Asp Thr Lys Ser Cys Leu Lys Asn Lys Thr Lys Glu Asn Val Asp	
125 130 135	
gtg ccc ctg gtc atc tgc ggc aac aag ggt gac cgc gac ttc tac cgc	604
Val Pro Leu Val Ile Cys Gly Asn Lys Gly Asp Arg Asp Phe Tyr Arg	
140 145 150	
gag gtg gac cag cgc gag atc gag cag ctg gtg ggc gac gac ccc cag	652
Glu Val Asp Gln Arg Glu Ile Glu Gln Leu Val Gly Asp Asp Pro Gln	
155 160 165	
cgc tgc gcc tac ttc gag atc tgc gcc aag aag aac agc agc ctg gac	700
Arg Cys Ala Tyr Phe Glu Ile Ser Ala Lys Lys Asn Ser Ser Leu Asp	
170 175 180 185	
cag atg ttc cgc gcg ctc ttc gcc atg gcc aag ctg ccc agc gag atg	748
Gln Met Phe Arg Ala Leu Phe Ala Met Ala Lys Leu Pro Ser Glu Met	
190 195 200	
agc cca gac ctg cac cgc aag gtc tgc gtg cag tac tgc gac gtg ctg	796
Ser Pro Asp Leu His Arg Lys Val Ser Val Gln Tyr Cys Asp Val Leu	
205 210 215	
cac aag aag gcg ctg cgg aac aag aag ctg ctg cgg gcc ggc agc ggc	844
His Lys Lys Ala Leu Arg Asn Lys Lys Leu Leu Arg Ala Gly Ser Gly	
220 225 230	
ggc ggc ggc ggc gac ccg ggc gac gcc ttt ggc atc gtg gca ccc ttc	892
Gly Gly Gly Gly Asp Pro Gly Asp Ala Phe Gly Ile Val Ala Pro Phe	
235 240 245	
gcg cgc cgg ccc agc gta cac agc gac ctc atg tac atc cgc gag aag	940
Ala Arg Arg Pro Ser Val His Ser Asp Leu Met Tyr Ile Arg Glu Lys	
250 255 260 265	
gcc agc gcc ggc agc cag gcc aag gac aag gag cgc tgc gtc atc agc	988
Ala Ser Ala Gly Ser Gln Ala Lys Asp Lys Glu Arg Cys Val Ile Ser	
270 275 280	
taggagcccc gccgcgtgg cgacacaacc taaggaggac ctttttggtta agtcaaattcc	1048
aacggccccgg tgcgccccag gccgggagcg cgcgaggact ggcgtctccc ctccggcgga	1108
tccgccccca gcaactgggga gccgccactg aaccogagaag ggacgggtcat ctgctccgga	1168
aggaaagaga acggggccaag actgggacta ttccccaccc ccggtccccc attgaggccc	1228
gccacccccca taactttggg agcgagggcc cagccgaggg tggattttatc ttctcaaaga	1288
cctaagagtg agcgcgggggt ggggggagga tgtgaagtta tccagcctct gctaggcttc	1348

aagaaaccgt catgcccgct tgaggggtcag gacccacggg gcattatctt gtctgtgatt 1408  
ccgggttgct gtgacagccg gtagagcctc tgcctcccg aaactaagcg ggggggcgtg 1468  
gggtcaaata tagccaagtg acttggtttac atgtgagtga aactgcacaa aggaacacaa 1528  
aacaaaactt gcactttaac ggtagttccg gtgtcaacat ggacacgaac aaaaccttac 1588  
ccagggtgttt atactgtgtg tgtgtgaggt ctttaaagtt attgctttat ttgggttttt 1648  
aatatacaat aaaataattt aaaatggaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1708  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1740

<210> 46

<211> 281

<212> PRT

<213> Homo Sapiens

<400> 46

Met Lys Leu Ala Ala Met Ile Lys Lys Met Cys Pro Ser Asp Ser Glu  
1 5 10 15

Leu Ser Ile Pro Ala Lys Asn Cys Tyr Arg Met Val Ile Leu Gly Ser  
20 25 30

Ser Lys Val Gly Lys Thr Ala Ile Val Ser Arg Phe Leu Thr Gly Arg  
35 40 45

Phe Glu Asp Ala Tyr Thr Pro Thr Ile Glu Asp Phe His Arg Lys Phe  
50 55 60

Tyr Ser Ile Arg Gly Glu Val Tyr Gln Leu Asp Ile Leu Asp Thr Ser  
65 70 75 80

Gly Asn His Pro Phe Pro Ala Met Arg Arg Leu Ser Ile Leu Thr Gly  
85 90 95

Asp Val Phe Ile Leu Val Phe Ser Leu Asp Asn Arg Asp Ser Phe Glu  
100 105 110

Glu Val Gln Arg Leu Arg Gln Gln Ile Leu Asp Thr Lys Ser Cys Leu  
115 120 125

Lys Asn Lys Thr Lys Glu Asn Val Asp Val Pro Leu Val Ile Cys Gly  
130 135 140

Asn Lys Gly Asp Arg Asp Phe Tyr Arg Glu Val Asp Gln Arg Glu Ile  
145 150 155 160

Glu Gln Leu Val Gly Asp Asp Pro Gln Arg Cys Ala Tyr Phe Glu Ile  
165 170 175

Ser Ala Lys Lys Asn Ser Ser Leu Asp Gln Met Phe Arg Ala Leu Phe  
180 185 190

Ala Met Ala Lys Leu Pro Ser Glu Met Ser Pro Asp Leu His Arg Lys  
195 200 205

Val Ser Val Gln Tyr Cys Asp Val Leu His Lys Lys Ala Leu Arg Asn  
210 215 220

Lys Lys Leu Leu Arg Ala Gly Ser Gly Gly Gly Gly Asp Pro Gly  
225 230 235 240

Asp Ala Phe Gly Ile Val Ala Pro Phe Ala Arg Arg Pro Ser Val His  
245 250 255

Ser Asp Leu Met Tyr Ile Arg Glu Lys Ala Ser Ala Gly Ser Gln Ala  
260 265 270

Lys Asp Lys Glu Arg Cys Val Ile Ser  
275 280

<210> 47

<211> 189

<212> PRT

<213> Homo Sapiens

<400> 47

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys  
1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr  
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly  
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr  
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys  
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr  
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val  
100 105 110

Leu Val Gly Asn Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg  
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr  
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val  
145 150 155 160

Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu  
165 170 175

Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser  
180 185

<210> 48

<211> 206

<212> PRT

<213> Homo Sapiens

<400> 48

Met Ala Ala Asn Lys Pro Lys Gly Gln Asn Ser Leu Ala Leu His Lys  
1 5 10 15

Val Ile Met Val Gly Ser Gly Gly Val Gly Lys Ser Ala Leu Thr Leu  
20 25 30

Gln Phe Met Tyr Asp Glu Phe Val Glu Asp Tyr Glu Pro Thr Lys Ala  
35 40 45

Asp Ser Tyr Arg Lys Lys Val Val Leu Asp Gly Glu Glu Val Gln Ile  
50 55 60

Asp Ile Leu Asp Thr Ala Gly Gln Glu Asp Tyr Ala Ala Ile Arg Asp  
65 70 75 80

Asn Tyr Phe Arg Ser Gly Glu Gly Phe Leu Cys Val Phe Ser Ile Thr  
85 90 95

Glu Met Glu Ser Phe Ala Ala Thr Ala Asp Phe Arg Glu Gln Ile Leu  
100 105 110

Arg Val Lys Glu Asp Glu Asn Val Pro Phe Leu Leu Val Gly Asn Lys  
115 120 125

Ser Asp Leu Glu Asp Lys Arg Gln Val Ser Val Glu Glu Ala Lys Asn  
130 135 140

Arg Ala Glu Gln Trp Asn Val Asn Tyr Val Glu Thr Ser Ala Lys Thr  
145 150 155 160

Arg Ala Asn Val Asp Lys Val Phe Phe Asp Leu Met Arg Glu Ile Arg  
165 170 175

Ala Arg Lys Met Glu Asp Ser Lys Glu Lys Asn Gly Lys Lys Lys Arg  
180 185 190

Lys Ser Leu Ala Lys Arg Ile Arg Glu Arg Cys Cys Ile Leu  
195 200 205

<210> 49

<211> 205

<212> PRT

<213> Homo Sapiens

<400> 49

Met Ser Ser Met Asn Pro Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu  
1 5 10 15

Ile Gly Asp Ser Gly Val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ala  
20 25 30

Asp Asp Thr Tyr Thr Glu Ser Tyr Ile Ser Thr Ile Gly Val Asp Phe  
35 40 45



Lys Ile Arg Thr Ile Glu Leu Asp Gly Lys Thr Ile Lys Leu Gln Ile  
50 55 60

Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Ser Tyr  
65 70 75 80

Tyr Arg Gly Ala His Gly Ile Ile Val Val Tyr Asp Val Thr Asp Gln  
85 90 95

Glu Ser Phe Asn Asn Val Lys Gln Trp Leu Gln Glu Ile Asp Arg Tyr  
100 105 110

Ala Ser Glu Asn Val Asn Lys Leu Leu Val Gly Asn Lys Cys Asp Leu  
115 120 125

Thr Thr Lys Lys Val Val Asp Tyr Thr Thr Ala Lys Glu Phe Ala Asp  
130 135 140

Ser Leu Gly Ile Pro Phe Leu Glu Thr Ser Ala Lys Asn Ala Thr Asn  
145 150 155 160

Val Glu Gln Ser Phe Met Thr Met Ala Ala Glu Ile Lys Lys Arg Met  
165 170 175

Gly Pro Gly Ala Thr Ala Gly Gly Ala Glu Lys Ser Asn Val Lys Ile  
180 185 190

Gln Ser Thr Pro Val Lys Gln Ala Gly Gly Gly Cys Cys  
195 200 205

<210> 50

<211> 210

<212> PRT

<213> Homo Sapiens

<400> 50

Met Thr Ala Ala Gln Ala Ala Gly Glu Glu Ala Pro Pro Gly Val Arg  
1 5 10 15

Ser Val Lys Val Val Leu Val Gly Asp Gly Gly Cys Gly Lys Thr Ser  
20 25 30

Leu Leu Met Val Phe Ala Asp Gly Ala Phe Pro Glu Ser Tyr Thr Pro  
35 40 45

Thr Val Phe Glu Arg Tyr Met Val Asn Leu Gln Val Lys Gly Lys Pro  
50 55 60

Val His Leu His Ile Trp Asp Thr Ala Gly Gln Asp Asp Tyr Asp Arg  
65 70 75 80

Leu Arg Pro Leu Phe Tyr Pro Asp Ala Ser Val Leu Leu Leu Cys Phe  
85 90 95

Asp Val Thr Ser Pro Asn Ser Phe Asp Asn Ile Phe Asn Arg Trp Tyr  
100 105 110

Pro Glu Val Asn His Phe Cys Lys Lys Val Pro Ile Ile Val Val Gly  
115 120 125

Cys Lys Thr Asp Leu Arg Lys Asp Lys Ser Leu Val Asn Lys Leu Arg  
130 135 140

Arg Asn Gly Leu Glu Pro Val Thr Tyr His Arg Gly Gln Glu Met Ala  
145 150 155 160

Arg Ser Val Gly Ala Val Ala Tyr Leu Glu Cys Ser Ala Arg Leu His  
165 170 175

Asp Asn Val His Ala Val Phe Gln Glu Ala Ala Glu Val Ala Leu Ser  
180 185 190

Ser Arg Gly Arg Asn Phe Trp Arg Arg Ile Thr Gln Gly Phe Cys Val  
195 200 205

Val Thr  
210

<210> 51

<211> 191

<212> PRT

<213> Homo Sapiens

<400> 51

Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys  
1 5 10 15

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser Glu Tyr  
20 25 30

Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile Gly Gly  
35 40 45

Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu Asp Tyr  
50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe Leu Val  
65 70 75 80

Cys Phe Ser Val Val Ser Pro Ser Ser Phe Glu Asn Val Lys Glu Lys  
85 90 95

Trp Val Pro Glu Ile Thr His His Cys Pro Lys Thr Pro Phe Leu Leu  
100 105 110

Val Gly Thr Gln Ile Asp Leu Arg Asp Asp Pro Ser Thr Ile Glu Lys  
115 120 125

Leu Ala Lys Asn Lys Gln Lys Pro Ile Thr Pro Glu Thr Ala Glu Lys  
130 135 140

Leu Ala Arg Asp Leu Lys Ala Val Lys Tyr Val Glu Cys Ser Ala Leu  
145 150 155 160

Thr Gln Arg Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu Ala Ala  
165 170 175

Leu Glu Pro Pro Glu Thr Gln Pro Lys Arg Lys Cys Cys Ile Phe  
180 185 190

<210> 52

<211> 192

<212> PRT

<213> Homo Sapiens

<400> 52

Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys  
1 5 10 15

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly Glu Tyr  
20 25 30

Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val Asp Ser  
35 40 45

Lys Pro Val Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr  
50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe Leu Ile  
65 70 75 80

Cys Phe Ser Leu Val Ser Pro Ala Ser Tyr Glu Asn Val Arg Ala Lys  
85 90 95

Trp Phe Pro Glu Val Arg His His Cys Pro Ser Thr Pro Ile Ile Leu  
100 105 110

Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys Asp Thr Ile Glu Lys  
115 120 125

Leu Lys Glu Lys Lys Leu Ala Pro Ile Thr Tyr Pro Gln Gly Leu Ala  
130 135 140

Leu Ala Lys Glu Ile Asp Ser Val Lys Tyr Leu Glu Cys Ser Ala Leu  
145 150 155 160

Thr Gln Arg Gly Leu Lys Thr Val Phe Asp Glu Ala Ile Arg Ala Val  
165 170 175

Leu Cys Pro Gln Pro Thr Arg Gln Gln Lys Arg Ala Cys Ser Leu Leu  
180 185 190

<210> 53

<211> 181

<212> PRT

<213> Homo Sapiens

<400> 53

Met Gly Gly Phe Phe Ser Ser Ile Phe Ser Ser Leu Phe Gly Thr Arg  
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Glu Met Arg Ile Leu Ile Leu Gly Leu Asp Gly Ala Gly Lys Thr Thr  
20 25 30

Ile Leu Tyr Arg Leu Gln Val Gly Glu Val Val Thr Thr Ile Pro Thr  
35 40 45

Ile Gly Phe Asn Val Glu Thr Val Thr Tyr Lys Asn Leu Lys Phe Gln  
50 55 60

Val Trp Asp Leu Gly Gly Gln Thr Ser Ile Arg Pro Tyr Trp Arg Cys  
65 70 75 80

Tyr Tyr Ser Asn Thr Asp Ala Val Ile Tyr Val Val Asp Ser Cys Asp  
85 90 95

Arg Asp Arg Ile Gly Ile Ser Lys Ser Glu Leu Val Ala Met Leu Glu  
100 105 110

Glu Glu Glu Leu Arg Lys Ala Ile Leu Val Val Phe Ala Asn Lys Gln  
115 120 125

Asp Met Glu Gln Ala Met Thr Ser Ser Glu Met Ala Asn Ser Leu Gly  
130 135 140

Leu Pro Ala Leu Lys Asp Arg Lys Trp Gln Ile Phe Lys Thr Ser Ala  
145 150 155 160

Thr Lys Gly Thr Gly Leu Asp Glu Ala Met Glu Trp Leu Val Glu Thr  
165 170 175

Leu Lys Ser Arg Gln  
180

<210> 54

<211> 229

<212> PRT

<213> Homo Sapiens

<400> 54

Met Asp Pro Asn Gln Asn Val Lys Cys Lys Ile Val Val Val Gly Asp  
 1 5 10 15  
 Ser Gln Cys Gly Lys Thr Ala Leu Leu His Val Phe Ala Lys Asp Cys  
 20 25 30  
 Phe Pro Glu Asn Tyr Val Pro Thr Val Phe Glu Asn Tyr Thr Ala Ser  
 35 40 45  
 Phe Glu Ile Asp Thr Gln Arg Ile Glu Leu Ser Leu Trp Asp Thr Ser  
 50 55 60  
 Gly Ser Pro Tyr Tyr Asp Asn Val Arg Pro Leu Ser Tyr Pro Asp Ser  
 65 70 75 80  
 Asp Ala Val Leu Ile Cys Phe Asp Ile Ser Arg Pro Glu Thr Leu Asp  
 85 90 95  
 Ser Val Leu Lys Lys Trp Lys Gly Glu Ile Gln Glu Phe Cys Pro Asn  
 100 105 110  
 Thr Lys Met Leu Leu Val Gly Cys Lys Ser Asp Leu Arg Thr Asp Val  
 115 120 125  
 Ser Thr Leu Val Glu Leu Ser Asn His Arg Gln Thr Pro Val Ser Tyr  
 130 135 140  
 Asp Gln Gly Ala Asn Met Ala Lys Gln Ile Gly Ala Ala Thr Tyr Ile  
 145 150 155 160  
 Glu Cys Ser Ala Leu Gln Ser Glu Asn Ser Val Arg Asp Ile Phe His  
 165 170 175  
 Val Ala Thr Leu Ala Cys Val Asn Lys Thr Asn Lys Asn Val Lys Arg  
 180 185 190  
 Asn Lys Ser Gln Arg Ala Thr Lys Arg Ile Ser His Met Pro Ser Arg  
 195 200 205  
 Pro Glu Leu Ser Ala Val Ala Thr Asp Leu Arg Lys Asp Lys Ala Lys  
 210 215 220  
 Ser Cys Thr Val Met  
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<210> 55

<211> 16

<212> PRT

<213> Homo Sapiens

<400> 55

Lys Ile Val Val Val Gly Asp Ser Gln Cys Gly Lys Thr Ala Leu Leu  
1 5 10 15

<210> 56

<211> 16

<212> PRT

<213> Homo Sapiens

<400> 56

Lys Ile Val Val Val Gly Asp Ala Glu Cys Gly Lys Thr Ala Leu Leu  
1 5 10 15

<210> 57

<211> 16

<212> PRT

<213> Homo Sapiens

<400> 57

Lys Leu Val Leu Val Gly Asp Val Gln Cys Gly Lys Thr Ala Met Leu  
1 5 10 15

<210> 58

<211> 16

<212> PRT

<213> Homo Sapiens

<400> 58

Lys Leu Val Ile Val Gly Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu  
1 5 10 15

<210> 59

<211> 16

<212> PRT

<213> Homo Sapiens

<400> 59

Lys Leu Val Val Val Gly Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu  
1 5 10 15

<210> 60

<211> 16

<212> PRT

<213> Homo Sapiens

<400> 60

Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys Leu Leu  
1 5 10 15

<210> 61

<211> 16

<212> PRT

<213> Homo Sapiens

<400> 61

Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys Leu Leu  
1 5 10 15

<210> 62

<211> 16

<212> PRT

<213> Homo Sapiens



<400> 62

Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys Ser Ala Leu Thr  
1 5 10 15

<210> 63

<211> 16

<212> PRT

<213> Homo Sapiens

<400> 63

Arg Met Val Ile Leu Gly Ser Ser Lys Val Gly Lys Thr Ala Ile Val  
1 5 10 15

<210> 64

<211> 13

<212> PRT

<213> Homo Sapiens

<400> 64

Leu Ser Leu Trp Asp Thr Ser Gly Ser Pro Tyr Tyr Asp  
1 5 10

<210> 65

<211> 13

<212> PRT

<213> Homo Sapiens

<400> 65

Leu Asn Met Trp Asp Thr Ser Gly Ser Ser Tyr Tyr Asp  
1 5 10

<210> 66

<211> 13

<212> PRT

<213> Homo Sapiens

<400> 66

Leu Ser Leu Trp Asp Thr Ser Gly Ser Pro Tyr Tyr Asp  
1 5 10

<210> 67

<211> 13

<212> PRT

<213> Homo Sapiens

<400> 67

Leu Ala Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr Asp  
1 5 10

<210> 68

<211> 13

<212> PRT

<213> Homo Sapiens

<400> 68

Leu Ala Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr Asp  
1 5 10

<210> 69

<211> 13

<212> PRT

<213> Homo Sapiens

<400> 69

Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu Asp Tyr Asp  
1 5 10

<210> 70

<211> 13

<212> PRT

<213> Homo Sapiens

<400> 70

Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr Asp  
1 5 10

<210> 71

<211> 13

<212> PRT

<213> Homo Sapiens

<400> 71

Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr Asp  
1 5 10

<210> 72

<211> 13

<212> PRT

<213> Homo Sapiens

<400> 72

Leu Asp Ile Leu Asp Thr Ser Gly Asn His Pro Phe Pro  
1 5 10

<210> 73

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Probe/Primer

<400> 73

ctcatggagc tcaaactgtt actattaggt gccg

34